

CLAIMS

We claim:

- 5 1. A method for detecting a target sequence, comprising:
- a) providing:
- i) a sample suspected of containing said target sequence;
- ii) oligonucleotides capable of forming an invasive cleavage
 structure in the presence of said target sequence; and
- 10 iii) an agent for detecting the presence of an invasive cleavage
 structure; and
- b) exposing said sample to said oligonucleotides and said agent.
2. The method of Claim 1, wherein said agent comprises a cleavage agent.
- 15 3. The method of Claim 2, wherein said exposing said sample to said
 oligonucleotides and said agent comprises exposing said sample to said oligonucleotides
 and said agent under conditions wherein an invasive cleavage structure is formed
 between said target sequence and said oligonucleotides if said target sequence is present
- 20 in said sample, wherein said invasive cleavage structure is cleaved by said cleavage agent
 to form a cleavage product.
4. The method of Claim 3, further comprising the step of c) detecting said
 cleavage product.
- 25 5. The method of Claim 1, wherein said target sequence comprises a first
 region and a second region, said second region downstream of and contiguous to said
 first region, and wherein said oligonucleotides comprise first and second
 oligonucleotides, said wherein at least a portion of said first oligonucleotide is completely
- 30 complementary to said first portion of said target sequence and wherein said second

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oligonucleotide comprises a 3' portion and a 5' portion, wherein said 5' portion is completely complementary to said second portion of said target nucleic acid.

5 6. The method of Claim 1, wherein said target sequence is selected from the group consisting of human cytomegalovirus viral DNA; polymorphisms in human apolipoprotein E gene; mutations in human hemochromatosis gene; mutations in human MTHFR; prothrombin 20210GA polymorphism; HR-2 mutation in human factor V gene; single nucleotide polymorphisms in human TNF- α gene, and Leiden mutation in human factor V gene.

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7. A kit for detecting a target sequence comprising oligonucleotides capable of forming an invasive cleavage structure in the presence of said target sequence.

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8. The kit of Claim 7, further comprising an agent for detecting the presence of an invasive cleavage structure.

9. The kit of Claim 8, wherein said agent comprises a cleavage agent.

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10. The kit of Claim 7, wherein said oligonucleotides comprise first and second oligonucleotides, said first oligonucleotide comprising a 5' portion complementary to a first region of said target nucleic acid and said second oligonucleotide comprising a 3' portion and a 5' portion, said 5' portion complementary to a second region of said target nucleic acid downstream of and contiguous to said first portion of said target nucleic acid.

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11. The kit of Claim 7, wherein said target sequence is selected from the group consisting of human cytomegalovirus viral DNA; polymorphisms in human apolipoprotein E gene; mutations in human hemochromatosis gene; mutations in human MTHFR; prothrombin 20210GA polymorphism; HR-2 mutation in human factor V gene; single nucleotide polymorphisms in human TNF- α gene, and Leiden mutation in human factor V gene.

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